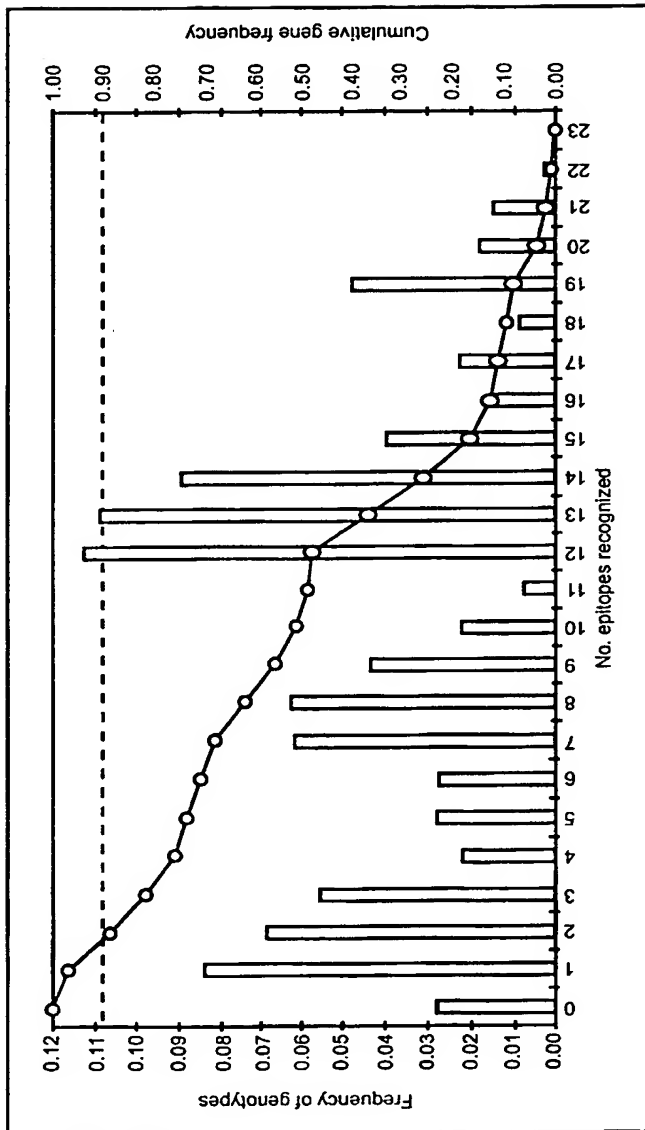


1 / 2

Monte Carlo population coverage analysis for HCV candidate epitopes



Plot of total frequency of genotypes as a function of the number of HCV candidate epitopes bound by HLA-A and B alleles, in an average population. Genotype values were derived by averaging the gene frequencies in Caucasian, North American, Black, Japanese, Chinese, and Hispanic populations. Also shown is the cumulative frequency of genotypes.

Using currently available HLA typing data, a residual fraction (about 15%) of the genes, in an average population, are unspecified. To arrive at 100% accounting of genes, a fraction of the residual has been added for each hit population cluster in proportion to the relative frequency of the cluster within the HLA specified population. One peptide, 24.0086, was not incorporated into the present analysis.

FIG. 1

HVC Minigene

CTL Epitopes

| | | | | | | | | | |
|---------|--------|----------|----------|----------|----------|------------|----------|----------|----------|
| Core 43 | | NS4 1590 | NS3 1128 | NS5 2611 | Core 169 | NS1/E2 632 | NS4 1765 | NS4 1863 | Core 132 |
| Kozak | SigSeq | 1073.11 | 1013.02 | 1069.62 | 1090.02 | 1145.12 | 1073.13 | 24.0092 | 1073.10 |
| A3 | | A2 | A1 | A2 | B7 | A3 | A24 | A3 | A2 |

| | | | | |
|----------|----------|---------|----------|---------|
| NS3 1253 | NS4 1921 | 1437 | NS5 2641 | 1466 |
| 1283.21 | 1283.44 | 35.0106 | 1283.55 | 35.0107 |
| DR | DR | DR3 | DR | DR3 |

HTL Epitopes

FIG. 2